In the Specification:

Please replace the paragraph on page 1, lines 2-3 with the following:

This application is a divisional application and claims benefit under 35 U.S.C. §120 of U.S. Application No. 09/877,476, filed June 8, 2001, which claims benefit under 35 U.S.C. §119(e) of U.S. Application No. 60/210,326, filed June 8, 2000.

Please amend the paragragh bridging pages 9 and 10 as follows:

The above-described polypeptides include a first polypeptide segment that can serve as a membrane anchor. Such a segment has properties that result in the elongase KCS polypeptide being anchored to a membrane, such as a lipid bilayer, detergent bilayer, micelle, or cell membrane. Possession of membrane anchoring properties may be the result of the primary structure, secondary structure and/or tertiary structure of the segment. For example, the segment may contain one or more transmembrane domain(s). Alternatively, a post-translational modification of an amino acid residue within the segment can result in the polypeptide being anchored to a membrane. Suitable modifications include, but are not limited to, covalent attachment of a lipid (*e.g.*, a glycosyl phosphatidylinositol anchor) or a carbohydrate (*e.g.*, an oligosaccharide). See, Alberts et al., *The Cell*, 2nd Edition, Garland Publishing, New York, pp 284-298 and Lodish et al., *Molecular Cell Biology*, 3rd Edition, Scientific American Books, p. 604 and pp. 688-692. The ability of a segment to serve as a membrane anchor can be demonstrated by observing whether a polypeptide having such a segment co-purifies with a membrane fraction. Alternatively, a segment can be a membrane-anchor if, after fusing it to the second and third segments, it is shown that the polypeptide possesses elongase KCS activity in an *in vitro* yeast microsome assay, since elongase KCS polypeptides are active when anchored to a membrane. As another alternative, computer algorithms, such as Predict Protein or META Predict Protein ~~(see www.embl-heidelberg.de/predictprotein)~~, can be used to predict the presence of a transmembrane domain within a segment, and hence, the ability of that polypeptide segment to serve as a membrane anchor.

Please amend the paragraph on page 10, lines 18-28 as follows:

A percent identity for any subject nucleic acid or amino acid sequence (*e.g.,* any of the fatty acid elongase chimeras described herein) relative to another "target" nucleic acid or amino acid sequence can be determined as follows. First, a target nucleic acid or amino acid sequence of the invention can be compared and aligned to a subject nucleic acid or amino acid sequence, preferably using the BLAST 2 Sequences (Bl2seq) program from the stand-alone version of BLASTZ containing BLASTN and BLASTP (*e.g.,* version 2.0.14). The stand-alone version of BLASTZ can be obtained at <u>Fish & Richardson's website or the National Center for Biotechnology Information (NCBI) website</u> <s><www.fr.com></s> <s>or <www.ncbi.nlm.nih.gov></s>. Instructions explaining how to use BLASTZ, and specifically the Bl2seq program, can be found in the 'readme' file accompanying BLASTZ. The programs also are described in detail by Karlin et al. (*Proc. Natl. Acad. Sci. USA,* 87:2264 (1990) and 90:5873 (1993)) and Altschul et al. (*Nucl. Acids Res.,* 25:3389 (1997)).

Please replace the Sequence Listing in the application with the Sequence Listing filed herewith.